

SEQUENCE LISTING

<110> Glucksmann, Maria A.

<120> 14273 Receptor, A Novel G-Protein Coupled Receptor

<130> 5800-4B, 035800/177086

<140> 09/261,599

<141> 1999-02-26

<150> 09/107,761

<151> 1998-06-30

<150> 09/223,538

<151> 1998-12-30

<160> 7

<170> PatentIn Ver. 2.1

<210> 1

<211> 361

<212> PRT

<213> Homo sapiens

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Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys
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Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val
35 40 45

Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
50 55 60

Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn
65 70 75 80

Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
85 90 95

Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
100 105 110

Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
115 120 125

Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln
130 135 140

Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala
145 150 155 160

Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe
165 170 175

Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser
180 185 190

Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp
195 200 205

Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
210 215 220

Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
225 230 235 240

Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
245 250 255

Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
260 265 270

Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
275 280 285

Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
290 295 300

Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
305 310 315 320

Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
325 330 335

Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys
340 345 350

Arg Asn Asp Leu Ser Ile Ile Ser Gly
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1005987.021302

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 <213> Homo sapiens

<400> 2

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 <213> Unknown

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<223> Description of Unknown Organism: Seven
 Transmembrane Segment Rhodopsin Superfamily

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Thr Pro Thr Asn Ile Phe Ile Leu Asn Leu Ala Val Ala Asp Leu Leu
20 25 30

Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly
35 40 45

Ser Glu Asp Trp Pro Phe Gly Ser Ala Leu Cys Lys Leu Val Thr Ala
50 55 60

Leu Asp Val Val Asn Met Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile
65 70 75 80

Ser Ile Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg
85 90 95

Arg Arg Thr Ser Pro Arg Arg Ala Lys Val Val Ile Leu Leu Val Trp
100 105 110

Val Leu Ala Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Val
115 120 125

Lys Thr Val Glu Glu Gly Asn Gly Thr Leu Asn Val Asn Val Thr Val
130 135 140

Cys Leu Ile Asp Phe Pro Glu Glu Ser Thr Ala Ser Val Ser Thr Trp
145 150 155 160

Leu Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu Pro
165 170 175

Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu Arg
180 185 190

Lys Ala Ala Lys Thr Leu Leu Val Val Val Val Val Phe Val Leu Cys
195 200 205

Trp Leu Pro Tyr Phe Ile Val Leu Leu Leu Asp Thr Leu Cys Leu Ser
210 215 220

Ile Ile Met Ser Ser Thr Cys Glu Leu Glu Arg Val Leu Pro Thr Ala
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Ile Ile Tyr

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<213> Murine ortholog

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20

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30

Gly Asp His Arg Leu Val Leu Ser Val Val Glu Thr Thr Val Leu Gly

35

40

45

Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu

50

55

60

Val Ala Arg Arg Arg Arg Arg Gly Ala Ser Ala Ser Leu Val Leu Asn

65

70

75

80

Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile Pro Leu Val Leu

85

90

95

Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Val Cys His

100

105

110

Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val Thr Ile Leu Thr

115

120

125

Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val Arg Leu Arg

130

135

140

Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala Leu Leu Ala

145

150

155

160

Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu Tyr Ile Leu

165

170

175

Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln Glu Ile Pro

180

185

190

Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile Ser Trp Asp

195

200

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Val Phe Phe Glu Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
210 215 220

Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
225 230 235 240

Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
245 250 255

Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
260 265 270

Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
275 280 285

Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
290 295 300

Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
305 310 315 320

Tyr Asn Met Ser Leu Phe Arg Asn Glu Trp Arg Lys Ile Phe Cys Cys
325 330 335

Phe Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Asp Thr Ser Val Arg
340 345 350

Arg Asn Asp Leu Ser Val Ile Ser Ser
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<210> 5

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<212> DNA

<213> Murine ortholog

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<211> 300

<212> PRT

<213> Homo sapiens

<220>

<223> mature polypeptide of 14273

<400> 6

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Val Leu Asn Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro
20 25 30

Leu Val Leu Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val
35 40 45

Ala Cys His Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr
50 55 60

Ile Leu Thr Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val
65 70 75 80

His Leu Gln Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val
85 90 95

Leu Leu Ala Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu
100 105 110

Cys Val Phe Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln
 115 120 125

Glu Ile Ser Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile
 130 135 140

Ser Trp Asp Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu
 145 150 155 160

Val Ile Val Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser
 165 170 175

Arg Lys Arg Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile
 180 185 190

Arg Val Ser Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu
 195 200 205

Met Val Ser Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu
 210 215 220

Leu Ile Leu Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser
 225 230 235 240

Leu Phe Phe Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn
 245 250 255

Pro Ile Leu Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile
 260 265 270

Phe Cys Cys Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr
 275 280 285

Ser Val Lys Arg Asn Asp Leu Ser Ile Ile Ser Gly
 290 295 300

<210> 7

<211> 300

<212> PRT

<213> Murine ortholog

<220>

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Leu Val Leu Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val	35	40	45
Val Cys His Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val Thr	50	55	60
Ile Leu Thr Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val	65	70	75
Arg Leu Arg Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala	85	90	95
Leu Leu Ala Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu	100	105	110
Tyr Ile Leu Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln	115	120	125
Glu Ile Pro Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile	130	135	140
Ser Trp Asp Val Phe Phe Glu Thr Leu Asn Phe Leu Val Pro Gly Leu	145	150	155
Val Ile Val Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser	165	170	175
Arg Lys Arg Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile	180	185	190
Arg Val Ser Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu	195	200	205
Met Val Ser Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu	210	215	220
Leu Ile Leu Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser	225	230	235
Leu Phe Phe Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn	245	250	255
Pro Ile Leu Tyr Asn Met Ser Leu Phe Arg Asn Glu Trp Arg Lys Ile			

260

265

270

Phe Cys Cys Phe Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Asp Thr
275 280 285

Ser Val Arg Arg Asn Asp Leu Ser Val Ile Ser Ser
290 295 300

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